

SEQUENCE LISTING

- (1) GENERAL INFORMATION:  
(i) APPLICANT: Li, ET AL.
- (ii) TITLE OF INVENTION: Human G-Protein Chemokine Receptor
- (iii) NUMBER OF SEQUENCES:
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
CECCHI, STEWART & OLSTEIN  
(B) STREET: 6 BECKER FARM ROAD  
(C) CITY: ROSELAND  
(D) STATE: NEW JERSEY  
(E) COUNTRY: USA  
(F) ZIP: 07068
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: 3.5 INCH DISKETTE  
(B) COMPUTER: IBM PS/2  
(C) OPERATING SYSTEM: MS-DOS  
(D) SOFTWARE: WORD PERFECT 5.1
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE: concurrently  
(C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: FERRARO, GREGORY D.  
(B) REGISTRATION NUMBER: 36,134  
(C) REFERENCE/DOCKET NUMBER: 325800-
- (viii) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 201-994-1700  
(B) TELEFAX: 201-994-1744
- (2) INFORMATION FOR SEQ ID NO:1
- (i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 1414 BASE PAIRS  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGAGATGGT GCTTTCATGA ATTCCCCCAA CAAGAGCCAA GCTCTCCATC TAGTGGACAG 60

GGAAGCTAGC AGCAAACCTT CCCTTCACTA CGAAACTCA TTGCTTGGCC CAAAAGAGAG 120  
 TTAATTCAAT GTAGACATCT ATGTAGGCAA TTAAAAACCT ATTGATGTAT AAAACAGTTT 180  
 GCATTCATGG AGGGCAACTA AATACATTCT AGGACTTTAT AAAAGATCAC TTTTTATTTA 240  
 TGCACAGGGT GGAACAAG ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC 291  
 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp  
 ATC AAT TAT TAT ACA TCG GAG CCC TGC CCA AAA ATC AAT GTG AAG CAA 339  
 Ile Asn Tyr Tyr Thr Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln  
 ATC GCA GCC CGC CTC CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT 387  
 Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe  
 GGT TTT GTG GGC AAC ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC CAA 435  
 Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Ile Asn Cys Gln  
 AGG CTG GAG AGC ATG ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT 483  
 Arg Leu Glu Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser  
 GAC CTG TTT TTC CTT CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC 531  
 Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala  
 GCC CAG TGG GAC TTT GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC 579  
 Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Leu Leu Thr Gly Leu Tyr  
 TAT TTT ATA GGC TTC TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA 627  
 Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Gln Leu Leu Thr  
 ATC GAT AGG TAC CTG GCT ATC GTC CAT GCT GTG TTT GCT TTA AAA GCC 675  
 Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala  
 AGG ACG GTC ACC TTT GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG 723  
 Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Val Val  
 GCT GTG TTT GCG TCT CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA 771  
 Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys  
 GAA GGT CTT CAT TAC ACC TGC AGC TGT CAT TTT CCA TAC AGT CAG TAT 819  
 Glu Gly Leu His Tyr Thr cys Ser Ser His Phe Pro Tyr Ser Gln Tyr  
 CAA TTC TGG AAG AAT TTC CAG ACA TTA AAG ATA GTC ATC TTG GGG CTG 867  
 Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu  
 GTC CTG CCG CTG CTT GTC ATG GTC ATC TGC TAC TCG GGA ATC CTA AAA 915  
 Val Leu Pro Leu Leu Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys  
 ACT CTG CTT CGG TGT CGA AAT GAG AAG AAG AGG CAC AGG GCT GTG AGG 963  
 Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg  
 CTT ATC TTC ACC ATC ATG ATT GTT TAT TTT CTC TTC TGG GCT CCC TAC 1011  
 Leu Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr  
 AAC ATT GTC CTT CTC CTG AAC ACC TTC CAG GAA TTC TTT GGC CTG AAT 1059  
 Asn Ile Val Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn  
 AAT TGC AGT AGC TCT AAC AGG TTG GAC CAA GCT ATG CAG GTG ACA GAG 1107  
 Asn Cys Ser Ser Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu  
 ACT CTT GGG ATG ACG CAC TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT 1155  
 Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe

GTC GGG GAG AAG TTC AGA AAC TAC CTC TTA GTC TTC TTC CAA AAG CAC 1203  
 Val Gly Glu Lys Phe Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His  
 ATT GCC AAA CGC TTC TGC AAA TGC TGT TCT ATT TTC CAG CAA GAG GCT 1251  
 Ile Ala Lys Arg Phe Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala  
 CCC GAG CGA GCA AGC TCA GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA 1299  
 Pro Glu Arg Ala Ser Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu  
 ATA TCT GTG GGC TTG TGACACGGAC TCAAGTGGGC TGGTGACCCA GTCAGAGTTG 1354  
 Ile Ser Val Gly Leu  
 TGCACATGGC TTAGTTTCA TACACAGCCT GGGCTGGGGG TGGGGTGGAA GAGGTCTTTT 1414

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: AMINO ACIDS
  - (B) TYPE: AMINO ACID
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr  
 5 10 15  
 Thr Ser Glu Pro Cys Pro Lys Ile Asn Val Lys Gln Ile Ala Ala  
 20 25 30  
 Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe  
 35 40 45  
 Val Gly Asn Met Leu Val Ile Leu Ile Ile Asn Cys Gln Arg  
 50 55 60  
 Leu Glu Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser  
 65 70 75  
 Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr Ala  
 80 85 90  
 Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Leu Leu Thr Gly  
 95 100 105  
 Leu Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Gln  
 110 115 120  
 Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe  
 125 130 135  
 Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val  
 140 145 150  
 Ile Thr Trp Val Val Ala Val Phe Ala Ser Leu Pro Gly Ile Ile  
 155 160 165  
 Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr Thr cys Ser Ser  
 170 175 180  
 His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn Phe Gln Thr  
 185 190 195  
 Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu Val Met  
 200 205 210

*Seb  
al  
cont*

Val	Ile	Cys	Tyr	Ser	Gly	Ile	Leu	Lys	Thr	Leu	Leu	Arg	Cys	Arg
				215					220					225
Asn	Glu	Lys	Lys	Arg	His	Arg	Ala	Val	Arg	Leu	Ile	Phe	Thr	Ile
				230					235					240
Met	Ile	Val	Tyr	Phe	Leu	Phe	Trp	Ala	Pro	Tyr	Asn	Ile	Val	Leu
				245					250					255
Leu	Leu	Asn	Thr	Phe	Gln	Glu	Phe	Phe	Gly	Leu	Asn	Asn	Cys	Ser
				260					265					270
Ser	Ser	Asn	Arg	Leu	Asp	Gln	Ala	Met	Gln	Val	Thr	Glu	Thr	Leu
				275					280					285
Gly	Met	Thr	His	Cys	Cys	Ile	Asn	Pro	Ile	Ile	Tyr	Ala	Phe	Val
				290					295					300
Gly	Glu	Lys	Phe	Arg	Asn	Tyr	Leu	Leu	Val	Phe	Phe	Gln	Lys	His
				305					310					315
Ile	Ala	Lys	Arg	Phe	Cys	Lys	Cys	Cys	Ser	Ile	Phe	Gln	Gln	Glu
				320					325					330
Ala	Pro	Glu	Arg	Ala	Ser	Ser	Val	Tyr	Thr	Arg	Ser	Thr	Gly	Glu
				335					340					345
Gln	Glu	Ile	Ser	Val	Gly	Leu								
				350										